RAW SEQUENCE LISTING

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Application Serial Number: _10/517,310_

Source: _PCT_

Date Processed by STIC: _10/25/2005_

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RAW SEQUENCE LISTING   DATE: 10/25/2005
PATENT APPLICATION: US/10/517,310   TIME: 12:04:15

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Output Set: N:\CRF4\10252005\J517310.raw

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 3 <110> APPLICANT: KOTANI, HIDEHITO
 4        MIZUARAI, SHINJI
 6 <120> TITLE OF INVENTION: METHOD FOR PREDICTING A DRUG TRANSPORT CAPABILITY BY ABCG2
 7        POLYMORPHISMS
 9 <130> FILE REFERENCE: 262507US0PCT
11 <140> CURRENT APPLICATION NUMBER: 10/517,310
12 <141> CURRENT FILING DATE: 2004-12-17
14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/07534
15 <151> PRIOR FILING DATE: 2003-06-13
17 <150> PRIOR APPLICATION NUMBER: JP 2002-175806
18 <151> PRIOR FILING DATE: 2002-06-17
20 <160> NUMBER OF SEQ ID NOS: 68
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1968
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(1965)
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37 1               5                   10                  15
39 acc aat ggc ttc ccc gcg aca gct tcc aat gac ctg aag gca ttt act        96
40 Thr Asn Gly Phe Pro Ala Thr Ala Ser Asn Asp Leu Lys Ala Phe Thr
41             20                  25                  30
43 gaa gga gct gtg tta agt ttt cat aac atc tgc tat cga gta aaa ctg        144
44 Glu Gly Ala Val Leu Ser Phe His Asn Ile Cys Tyr Arg Val Lys Leu
45         35                  40                  45
47 aag agt ggc ttt cta cct tgt cga aaa cca gtt gag aaa gaa ata tta        192
48 Lys Ser Gly Phe Leu Pro Cys Arg Lys Pro Val Glu Lys Glu Ile Leu
49     50                  55                  60
51 tcg aat atc aat ggg atc atg aaa cct ggt ctc aac gcc atc ctg gga        240
52 Ser Asn Ile Asn Gly Ile Met Lys Pro Gly Leu Asn Ala Ile Leu Gly
53 65                  70                  75                  80
55 ccc aca ggt gga ggc aaa tct tcg tta tta gat gtc tta gct gca agg        288
56 Pro Thr Gly Gly Gly Lys Ser Ser Leu Leu Asp Val Leu Ala Ala Arg
57                 85                  90                  95
59 aaa gat cca agt gga tta tct gga gat gtt ctg ata aat gga gca ccg        336
60 Lys Asp Pro Ser Gly Leu Ser Gly Asp Val Leu Ile Asn Gly Ala Pro
61             100                 105                 110
63 cga cct gcc aat ttc aaa tgt aat tca ggt tac gtg gta caa gat gat        384
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64 Arg Pro Ala Asn Phe Lys Cys Asn Ser Gly Tyr Val Val Gln Asp Asp
65         115                 120                 125
67 gtt gtg atg ggc act ctg acg gtg aga gaa aac tta cag ttc tca gca        432
68 Val Val Met Gly Thr Leu Thr Val Arg Glu Asn Leu Gln Phe Ser Ala
69     130                 135                 140
71 gct ctt cgg ctt gca aca act atg acg aat cat gaa aaa aac gaa cgg        480
72 Ala Leu Arg Leu Ala Thr Thr Met Thr Asn His Glu Lys Asn Glu Arg
73 145                 150                 155                 160
75 att aac agg gtc att caa gag tta ggt ctg gat aaa gtg gca gac tcc        528
76 Ile Asn Arg Val Ile Gln Glu Leu Gly Leu Asp Lys Val Ala Asp Ser
77                 165                 170                 175
79 aag gtt gga act cag ttt atc cgt ggt gtg tct gga gga gaa aga aaa        576
80 Lys Val Gly Thr Gln Phe Ile Arg Gly Val Ser Gly Gly Glu Arg Lys
81             180                 185                 190
83 agg act agt ata gga atg gag ctt atc act gat cct tcc atc ttg ttc        624
84 Arg Thr Ser Ile Gly Met Glu Leu Ile Thr Asp Pro Ser Ile Leu Phe
85             195                 200                 205
87 ttg gat gag cct aca act ggc tta gac tca agc aca gca aat gct gtc        672
88 Leu Asp Glu Pro Thr Thr Gly Leu Asp Ser Ser Thr Ala Asn Ala Val
89     210                 215                 220
91 ctt ttg ctc ctg aaa agg atg tct aag cag gga cga aca atc atc ttc        720
92 Leu Leu Leu Leu Lys Arg Met Ser Lys Gln Gly Arg Thr Ile Ile Phe
93 225                 230                 235                 240
95 tcc att cat cag cct cga tat tcc atc ttc aag ttg ttt gat agc ctc        768
96 Ser Ile His Gln Pro Arg Tyr Ser Ile Phe Lys Leu Phe Asp Ser Leu
97                 245                 250                 255
99 acc tta ttg gcc tca gga aga ctt atg ttc cac ggg cct gct cag gag        816
100 Thr Leu Leu Ala Ser Gly Arg Leu Met Phe His Gly Pro Ala Gln Glu
101             260                 265                 270
103 gcc ttg gga tac ttt gaa tca gct ggt tat cac tgt gag gcc tat aat        864
104 Ala Leu Gly Tyr Phe Glu Ser Ala Gly Tyr His Cys Glu Ala Tyr Asn
105             275                 280                 285
107 aac cct gca gac ttc ttc ttg gac atc att aat gga gat tcc act gct        912
108 Asn Pro Ala Asp Phe Phe Leu Asp Ile Ile Asn Gly Asp Ser Thr Ala
109     290                 295                 300
111 gtg gca tta aac aga gaa gaa gac ttt aaa gcc aca gag atc ata gag        960
112 Val Ala Leu Asn Arg Glu Glu Asp Phe Lys Ala Thr Glu Ile Ile Glu
113 305                 310                 315                 320
115 cct tcc aag cag gat aag cca ctc ata gaa aaa tta gcg gag att tat        1008
116 Pro Ser Lys Gln Asp Lys Pro Leu Ile Glu Lys Leu Ala Glu Ile Tyr
117             325                 330                 335
119 gtc aac tcc tcc ttc tac aaa gag aca aaa gct gaa tta cat caa ctt        1056
120 Val Asn Ser Ser Phe Tyr Lys Glu Thr Lys Ala Glu Leu His Gln Leu
121             340                 345                 350
123 tcc ggg ggt gag aag aag aag aag atc aca gtc ttc aag gag atc agc        1104
124 Ser Gly Gly Glu Lys Lys Lys Lys Ile Thr Val Phe Lys Glu Ile Ser
125             355                 360                 365
127 tac acc acc tcc ttc tgt cat caa ctc aga tgg gtt tcc aag cgt tca        1152
128 Tyr Thr Thr Ser Phe Cys His Gln Leu Arg Trp Val Ser Lys Arg Ser
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129    370                    375                   380
131 ttc aaa aac ttg ctg ggt aat ccc cag gcc tct ata gct cag atc att    1200
132 Phe Lys Asn Leu Leu Gly Asn Pro Gln Ala Ser Ile Ala Gln Ile Ile
133 385                    390                   395                   400
135 gtc aca gtc gta ctg gga ctg gtt ata ggt gcc att tac ttt ggg cta    1248
136 Val Thr Val Val Leu Gly Leu Val Ile Gly Ala Ile Tyr Phe Gly Leu
137                    405                   410                   415
139 aaa aat gat tct act gga atc cag aac aga gct ggg gtt ctc ttc ttc    1296
140 Lys Asn Asp Ser Thr Gly Ile Gln Asn Arg Ala Gly Val Leu Phe Phe
141                    420                   425                   430
143 ctg acg acc aac cag tgt ttc agc agt gtt tca gcc gtg gaa ctc ttt    1344
144 Leu Thr Thr Asn Gln Cys Phe Ser Ser Val Ser Ala Val Glu Leu Phe
145            435                   440                   445
147 gtg gta gag aag aag ctc ttc ata cat gaa tac atc agc gga tac tac    1392
148 Val Val Glu Lys Lys Leu Phe Ile His Glu Tyr Ile Ser Gly Tyr Tyr
149    450                    455                   460
151 aga gtg tca tct tat ttc ctt gga aaa ctg tta tct gat tta tta ccc    1440
152 Arg Val Ser Ser Tyr Phe Leu Gly Lys Leu Leu Ser Asp Leu Leu Pro
153 465                    470                   475                   480
155 atg agg atg tta cca agt att ata ttt acc tgt ata gtg tac ttc atg    1488
156 Met Arg Met Leu Pro Ser Ile Ile Phe Thr Cys Ile Val Tyr Phe Met
157                    485                   490                   495
159 tta gga ttg aag cca aag gca gat gcc ttc ttc gtt atg atg ttt acc    1536
160 Leu Gly Leu Lys Pro Lys Ala Asp Ala Phe Phe Val Met Met Phe Thr
161            500                   505                   510
163 ctt atg atg gtg gct tat tca gcc agt tcc atg gca ctg gcc ata gca    1584
164 Leu Met Met Val Ala Tyr Ser Ala Ser Ser Met Ala Leu Ala Ile Ala
165            515                   520                   525
167 gca ggt cag agt gtg gtt tct gta gca aca ctt ctc atg acc atc tgt    1632
168 Ala Gly Gln Ser Val Val Ser Val Ala Thr Leu Leu Met Thr Ile Cys
169    530                    535                   540
171 ttt gtg ttt atg atg att ttt tca ggt ctg ttg gtc aat ctc aca acc    1680
172 Phe Val Phe Met Met Ile Phe Ser Gly Leu Leu Val Asn Leu Thr Thr
173 545                    550                   555                   560
175 att gca tct tgg ctg tca tgg ctt cag tac ttc agc att cca cga tat    1728
176 Ile Ala Ser Trp Leu Ser Trp Leu Gln Tyr Phe Ser Ile Pro Arg Tyr
177                    565                   570                   575
179 gga ttt acg gct ttg cag cat aat gaa ttt ttg gga caa aac ttc tgc    1776
180 Gly Phe Thr Ala Leu Gln His Asn Glu Phe Leu Gly Gln Asn Phe Cys
181            580                   585                   590
183 cca gga ctc aat gca aca gga aac aat cct tgt aac tat gca aca tgt    1824
184 Pro Gly Leu Asn Ala Thr Gly Asn Asn Pro Cys Asn Tyr Ala Thr Cys
185            595                   600                   605
187 act ggc gaa gaa tat ttg gta aag cag ggc atc gat ctc tca ccc tgg    1872
188 Thr Gly Glu Glu Tyr Leu Val Lys Gln Gly Ile Asp Leu Ser Pro Trp
189    610                    615                   620
191 ggc ttg tgg aag aat cac gtg gcc ttg gct tgt atg att gtt att ttc    1920
192 Gly Leu Trp Lys Asn His Val Ala Leu Ala Cys Met Ile Val Ile Phe
193 625                    630                   635                   640
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201 <211> LENGTH: 655
202 <212> TYPE: PRT
203 <213> ORGANISM: Homo sapiens
205 <400> SEQUENCE: 2
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212             20              25              30
215 Glu Gly Ala Val Leu Ser Phe His Asn Ile Cys Tyr Arg Val Lys Leu
216         35              40              45
219 Lys Ser Gly Phe Leu Pro Cys Arg Lys Pro Val Glu Lys Glu Ile Leu
220     50              55              60
223 Ser Asn Ile Asn Gly Ile Met Lys Pro Gly Leu Asn Ala Ile Leu Gly
224 65              70              75              80
227 Pro Thr Gly Gly Gly Lys Ser Ser Leu Leu Asp Val Leu Ala Ala Arg
228             85              90              95
231 Lys Asp Pro Ser Gly Leu Ser Gly Asp Val Leu Ile Asn Gly Ala Pro
232             100             105             110
235 Arg Pro Ala Asn Phe Lys Cys Asn Ser Gly Tyr Val Val Gln Asp Asp
236         115             120             125
239 Val Val Met Gly Thr Leu Thr Val Arg Glu Asn Leu Gln Phe Ser Ala
240         130             135             140
243 Ala Leu Arg Leu Ala Thr Thr Met Thr Asn His Glu Lys Asn Glu Arg
244 145             150             155             160
247 Ile Asn Arg Val Ile Gln Glu Leu Gly Leu Asp Lys Val Ala Asp Ser
248             165             170             175
251 Lys Val Gly Thr Gln Phe Ile Arg Gly Val Ser Gly Gly Glu Arg Lys
252         180             185             190
255 Arg Thr Ser Ile Gly Met Glu Leu Ile Thr Asp Pro Ser Ile Leu Phe
256         195             200             205
259 Leu Asp Glu Pro Thr Thr Gly Leu Asp Ser Ser Thr Ala Asn Ala Val
260     210             215             220
263 Leu Leu Leu Leu Lys Arg Met Ser Lys Gln Gly Arg Thr Ile Ile Phe
264 225             230             235             240
267 Ser Ile His Gln Pro Arg Tyr Ser Ile Phe Lys Leu Phe Asp Ser Leu
268             245             250             255
271 Thr Leu Leu Ala Ser Gly Arg Leu Met Phe His Gly Pro Ala Gln Glu
272             260             265             270
275 Ala Leu Gly Tyr Phe Glu Ser Ala Gly Tyr His Cys Glu Ala Tyr Asn
276         275             280             285
279 Asn Pro Ala Asp Phe Phe Leu Asp Ile Ile Asn Gly Asp Ser Thr Ala
280     290             295             300
283 Val Ala Leu Asn Arg Glu Glu Asp Phe Lys Ala Thr Glu Ile Ile Glu
284 305             310             315             320
287 Pro Ser Lys Gln Asp Lys Pro Leu Ile Glu Lys Leu Ala Glu Ile Tyr
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288                325                  330                  335
291 Val Asn Ser Ser Phe Tyr Lys Glu Thr Lys Ala Glu Leu His Gln Leu
292                340                  345                  350
295 Ser Gly Gly Glu Lys Lys Lys Lys Ile Thr Val Phe Lys Glu Ile Ser
296          355                  360                  365
299 Tyr Thr Thr Ser Phe Cys His Gln Leu Arg Trp Val Ser Lys Arg Ser
300      370                  375                  380
303 Phe Lys Asn Leu Leu Gly Asn Pro Gln Ala Ser Ile Ala Gln Ile Ile
304 385                  390                  395                  400
307 Val Thr Val Val Leu Gly Leu Val Ile Gly Ala Ile Tyr Phe Gly Leu
308                405                  410                  415
311 Lys Asn Asp Ser Thr Gly Ile Gln Asn Arg Ala Gly Val Leu Phe Phe
312                420                  425                  430
315 Leu Thr Thr Asn Gln Cys Phe Ser Ser Val Ser Ala Val Glu Leu Phe
316          435                  440                  445
319 Val Val Glu Lys Lys Leu Phe Ile His Glu Tyr Ile Ser Gly Tyr Tyr
320      450                  455                  460
323 Arg Val Ser Ser Tyr Phe Leu Gly Lys Leu Leu Ser Asp Leu Leu Pro
324 465                  470                  475                  480
327 Met Arg Met Leu Pro Ser Ile Ile Phe Thr Cys Ile Val Tyr Phe Met
328          485                  490                  495
331 Leu Gly Leu Lys Pro Lys Ala Asp Ala Phe Phe Val Met Met Phe Thr
332          500                  505                  510
335 Leu Met Met Val Ala Tyr Ser Ala Ser Ser Met Ala Leu Ala Ile Ala
336          515                  520                  525
339 Ala Gly Gln Ser Val Val Ser Val Ala Thr Leu Leu Met Thr Ile Cys
340      530                  535                  540
343 Phe Val Phe Met Met Ile Phe Ser Gly Leu Leu Val Asn Leu Thr Thr
344 545                  550                  555                  560
347 Ile Ala Ser Trp Leu Ser Trp Leu Gln Tyr Phe Ser Ile Pro Arg Tyr
348          565                  570                  575
351 Gly Phe Thr Ala Leu Gln His Asn Glu Phe Leu Gly Gln Asn Phe Cys
352          580                  585                  590
355 Pro Gly Leu Asn Ala Thr Gly Asn Asn Pro Cys Asn Tyr Ala Thr Cys
356          595                  600                  605
359 Thr Gly Glu Glu Tyr Leu Val Lys Gln Gly Ile Asp Leu Ser Pro Trp
360      610                  615                  620
363 Gly Leu Trp Lys Asn His Val Ala Leu Ala Cys Met Ile Val Ile Phe
364 625                  630                  635                  640
367 Leu Thr Ile Ala Tyr Leu Lys Leu Leu Phe Leu Lys Lys Tyr Ser
368          645                  650                  655
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372 <211> LENGTH: 18
373 <212> TYPE: DNA
374 <213> ORGANISM: Artificial Sequence
376 <220> FEATURE:
377 <223> OTHER INFORMATION: Synthetic DNA
379 <400> SEQUENCE: 3
380 gtgcccactc aaaaggtt                                              18
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/517,310**

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